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BLASTP 2.2.6 [Apr-09-2003]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query=

(114 letters)

Database: migallaseq

241 sequences; 23,537 total letters

Searching done

Sequences producing significant alignments:

	Score (bits)	E Value
J558.5	<u>183</u>	6e-50
45.21.1	<u>183</u>	6e-50
J558.11	<u>181</u>	3e-49
J558.3	<u>181</u>	3e-49
J558.2	<u>179</u>	8e-49
J558.8	<u>179</u>	8e-49
J558.4	<u>176</u>	7e-48
VH108A	<u>176</u>	9e-48
J558.1	<u>174</u>	2e-47
J558.12	<u>174</u>	2e-47
J558.6	<u>173</u>	4e-47
J558.7	<u>173</u>	4e-47
J558.1	<u>172</u>	8e-47
J558.9	<u>172</u>	8e-47
VH105	<u>168</u>	1e-46
J558.47	<u>168</u>	2e-45
J558.29	<u>163</u>	6e-44
V23	<u>163</u>	6e-44
J558.d	<u>163</u>	6e-44
J558.42	<u>162</u>	1e-43
V186.2	<u>162</u>	1e-43
VHF102	<u>161</u>	2e-43
J558.36	<u>161</u>	2e-43
J558.30	<u>159</u>	7e-43
J558.27	<u>159</u>	7e-43

SEQ ID No: 7  
in guideline ✓

Database: migallaseq  
 Posted date: Aug 27, 2002 4:57 PM  
 Number of letters in database: 23,537  
 Number of sequences in database: 241

Lambda K H  
 0.313 0.130 0.399

Gapped K H  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 16,624  
 Number of Sequences: 241  
 Number of extensions: 612  
 Number of successful extensions: 237  
 Number of sequences better than 1.0e-25: 101  
 Number of HSP's better than 0.0 without gapping: 99  
 Number of HSP's successfully gapped in prelim test: 2  
 Number of HSP's that attempted gapping in prelim test: 136  
 Number of HSP's gapped (non-prelim): 101  
 length of query: 114  
 length of database: 23,537  
 effective HSP length: 45  
 effective length of query: 69  
 effective length of database: 12,692  
 effective search space: 875748  
 effective search space used: 875748  
 T: 11  
 A: 40

X1: 16 ( 7.2 bits)  
 X2: 38 (14.6 bits)  
 X3: 64 (24.7 bits)  
 S1: 42 (21.9 bits)  
 S2: 255 (102.8 bits)

GL ID#	QUERY	1	EVQLQSGPDLVTPGASVKISCKASGYSFT	GYIYH	WKQSHGKSLIEWIG	RVIPNNGTSTY	60
ND							
89	J558.5*	1	.....E.....T..T..	E.TM.	.....GIN.....	60	
89	45.21.1*	1	.....E.....T..	D.MN	.....DIN.....	60	
87	J558.11*	1	.I.....E.M.....	S.M.	.....YID.F.....	60	

*Versus  
 germline  
 (exon 3)*

87	J558.3	1	.....E.....M.....T..D..MK	.....DIN.....	60
88	J558.2	1	.....E.....M.....T..D..MK	.....IN.Y.A...	60
86	J558.8	1	.....E.....M.....T..D..MK	.....LIN.Y..N..	60
85	J558.4	1	.....E.....M.....T..D..MK	.....DIN...D.F.	60
85	VH108A	1	.....E.....T..D..NM	.....YIY.Y...G.	60
84	J558.1	1	.....E.....V.....D..NMY	.....YID.Y.....	60
85	J558.12	1	.....E.E.....NMN	.....NID.YY...	60
85	J558.6	1	.....E.....P.....D..NMD	.....DIN.....I.	60
83	J558.7	1	.....F.E.LR.....M.....T..D..MD	.....E.F....	60
84	J558.1	1	.....E.E.T.....M.....M.	.....YISCY.A...	60
82	J558.9	1	.....E.....M.....TMN	.....N.D...LIN.YH...	60
77	VH105	1	.....E.....T..S....	.....YIY.RD.S.N.	60
79	J558.47	1	.....E.....M.....T..S.VM	.....YIN.Y.D.K.	60
77	J558.29	1	.....E.....R.....T..S....	.....WIIY.G.VN.K.	60
76	V23	1	.....P.TE.....L.....T..S.WM	.....NIN.S...N.	60
77	J558.d	2	.....P.AE.....L.....T..S.WM	.....ID.S...K.	60
77	J558.42	1	.....P.AE.....M.....T..S.NM	.....AIY.G.D...	60
77	V186.2	2	.....P.AE.....L.....T..S.WM	.....ID.S...K.	60
75	VHF102	1	.....E.....T..D..N	.....WIIY.GS.N.K.	60
76	J558.36	2	.....P.AE.....L.....T..S.WM	.....ID.S...K.	60
76	J558.30	1	.....E.....R.....F.T..S....	.....WIIY.G.VN.K.	60
75	J558.27	1	.....E.....M.....T..S....	.....WIIY.GD.S.K.	60
76	J558.m	1	.....E.....M.....T..D.VM	.....YIY.Y.D.E.	60
75	J558.33	1	.....P.AE.....L.....T..S.WM	.....EIN.S.R.N.	60
76	J558.35	1	.....AE.....L.....T..S.MY	.....EIN.S...NF	60

GL	ID	QUERY	61	NOIAPKG	KALITLWIDKSSSPAYMELRSLTASDASVYRGAR	98
ND		J558.5*	61	.....T.....	.....	98
		45.21.1*	61	.....T.....	.....	98
		J558.11*	61	.....T.....	.....	98
		J558.3	61	.....T.....	.....	98

	88	J558.2	61	.N.D	.S.....H.....	98
	86	J558.8	61	.....	.T.....L.....	98
	85	J558.4	61	.....	.T.....Q.N.....	98
	85	VH108A	61	.....S	.T...N.....S.....	98
	84	J558.1	61	.....	.T.....F.H.N.....	98
	85	J558.12	61	.....	.T.....Q.K.....	98
	85	J558.6	61	.....	.T.....T.....	98
	83	J558.7	61	.....	.T.A.....N.....	98
	84	J558.1	61	.....	.TF..T.....QFN.....	98
	82	J558.9	61	.....	.T.....T.L.....-	97
	77	VH105	61	.E....	.T.A.T.....Q.S.....F...	98
	79	J558.47	61	.E....	.T.S.....S.....	98
	77	J558.29	61	.E....	.T.A.....Q.S.....F...	98
	76	V23	61	.E..S	.T.....Q.S.....	98
	77	J558.d	61	.E..S	.T...P.....Q.S.....T.	98
	77	J558.42	61	.....	.T.A.....Q.S.....	98
	77	V186.2	61	.E..S	.T...P.....Q.S.....	98
	75	VHF102	61	.E....	.T...T.....Q.S.....T..F...	98
	76	J558.36	61	.E..S	.T...P.....Q.S.....T.	98
	76	J558.30	61	.E....	.T.A.....Q.S.....F...	98
	75	J558.27	61	.E....	.TT.A.....L.S.....I.F...	98
	76	J558.m	61	TE....	.T.L.....D.S.....T.....	98
	75	J558.33	61	.E..S	.T.....Q.S.....	98
	76	J558.35	61	.E..S	.T.....Q.S.....--	96

BLASTP 2.2.6 [Apr-09-2003]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Query=**

(114 letters)

**Database:** igSeqProt

32,732 sequences; 3,779,177 total letters

Searching done

Sequences producing significant alignments:

			Score E (bits) Value
gi 3561044	gb AAC35164.1	anti-HIV-1 p24 antibody D2 heavy ...	210 3e-56
gi 2895955	gb AAC03071.1	IgG1 heavy chain mAb1-1A [Mus mus...	204 2e-54
gi 3212408	pdb 1A6T D	Chain D, Fab Fragment Of Mabl-1a Mono...	204 2e-54
gi 3212406	pdb 1A6T B	Chain B, Fab Fragment Of Mabl-1a Mono...	204 2e-54
gi 33417043	gb AAH55910.1	Unknown (protein for MGC:68300) ...	201 1e-53
gi 22531696	dbj BAC10641.1	immunoglobulin gamma1 chain [Mus...	201 2e-53
gi 21304450	emb CAD32498.1	immunoglobulin gamma1 heavy cha...	200 3e-53
gi 21304449	emb CAD32497.1	immunoglobulin gamma1 heavy cha...	200 3e-53
gi 288838	emb CAA80023.1	immunoglobulin variable region [M...	199 5e-53
gi 194510	gb AAA51044.1	immunoglobulin gamma-1 chain	199 6e-53
gi 29725579	gb AAO89516.1	immunoglobulin heavy chain varia...	198 8e-53
gi 6688698	emb CAB65236.1	immunoglobulin heavy chain V-D-J...	198 8e-53
gi 2052431	gb AAB53405.1	anti-DNA antibody heavy chain var...	198 8e-53
gi 110101	pir I37267	Ig heavy chain V region (129) - mouse	197 2e-52
gi 34539550	gb AAQ74666.1	immunoglobulin mu heavy chain va...	196 3e-52
gi 6688700	emb CAB65237.1	immunoglobulin heavy chain V-D-J...	196 3e-52
gi 1407742	gb AAB03592.1	Ig heavy chain [Mus musculus]	196 3e-52
gi 123790	sp P01757 HV13	MOUSE IG HEAVY CHAIN V REGION J558	196 4e-52
gi 69903	pir MHMSJ75	Ig heavy chain V region (J558) - mouse...	196 4e-52
gi 193747	gb AAA37775.1	Ab 414.2 heavy chain variable and ...	196 4e-52
gi 5690323	gb AAD47037.1	immunoglobulin heavy chain variab...	195 7e-52
gi 297732	emb CAA80045.1	immunoglobulin variable region [M...	195 9e-52
gi 288818	emb CAA80085.1	immunoglobulin variable region [M...	194 1e-51
gi 309355	gb AAA38518.1	immunoglobulin heavy chain	194 1e-51
gi 193749	gb AAA37776.1	Ab 126.33 heavy chain variable and...	194 1e-51

SEQ ID No: 7  
in Ig

Database: igSeqProt  
Posted date: Oct 27, 2003 4:03 PM  
Number of letters in database: 3,779,177  
Number of sequences in database: 32,732

Lambda K H  
0.313 0.130 0.399

Gapped K H  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2,258,781

Number of Sequences: 32732

Number of extensions: 106964

Number of successful extensions: 48948

Number of sequences better than 1.0e-25: 250

Number of HSP's better than 0.0 without gapping: 7279

Number of HSP's successfully gapped in prelim test: 2159

Number of HSP's that attempted gapping in prelim test: 34534

Number of HSP's gapped (non-prelim): 9510

length of query: 114

length of database: 3,779,177

effective HSP length: 74

effective length of query: 40

effective length of database: 1,357,009

effective search space: 54280360

effective search space used: 54280360

T: 11

A: 40

X1: 16 ( 7.2 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (21.9 bits)

S2: 271 (109.0 bits)

GL	ID#	<-----FWRL----->	<CRL>	<-----FWR2----->	<-----CDR2		
ND	QUERY	1	EVOLQSGPDLVKPGASVKISCKASGYSFT	GYIHH	WVKOSHGKSLIEWIG	RVIPNNGTSTY	60
●	89	J558.5*	1	.....E.....T..T..	E.TM.	.....GIN.....	60
●	89	45.21.1*	1	.....E.....T..D..MN	.....DIN.....	.....	60
●	87	J558.11*	1	.I.....E.M.....	S.M.	.....YID.F.....	60
●	88	AAC35164	1	Q.....	..M.	.....N.....	60

86	AAC03071	1	.....	S	T.M.	.....	D.D.	60
86	1A6T D	1	.....	S	T.M.	.....	D.D.	60
86	1A6T B	1	.....	S	T.M.	.....	D.D.	60
83	AAH55910	20	.....	E.	.....	T.	M.	79
84	BAC10641	1	.....	E.	.....	T.	E.TM.	60
82	CAD32498	20	.....	ER.	.....	T.	D.MN	79
82	CAD32497	20	.....	ER.	.....	T.	D.MN	79
83	CAA80023	1	.....	E.	.....	D.	M.	60
85	AAA51044	4	.....	.....	.....	D.	L.	63
84	AAO89516	1	.....	E.	.....	D.	M.	59
82	CAB65236	1	.....	E.	.....	M.	T.	60
83	AAB53405	20	.....	E.	.....	T.	D.MN	79
79	I37267	6	.....	E.	.....	T.	E.TM.	64
87	AAQ74666	1	.....	.....	.....	.....	M.	52
81	CAB65237	1	.....	E.	.....	M.	T.	60
80	AAB03592	1	.....	E.	.....	.....	FMN	60
82	P01757	1	.....	E.	.....	M.	T.	60
82	MHMSJ5	1	.....	E.	.....	M.	T.	60
82	AAA37775	18	.....	E.	.....	M.	T.	77
81	AAD47037	1	.....	E.	.....	T.	E.TM.	60
79	CAA80045	1	.....	E.	.....	M.	T.	60
81	CAA80085	1	.....	E.	.....	M.	DS.MN	60
82	AAA38518	1	.....	E.	.....	D.	M.	60
82	AAA37776	18	.....	E.	.....	M.	T.	77
GL	ID#		----->	<-----	-----	-----	-----	
ND	QUERY	61	NOKFKG	KALITVDKSSSTAYMELRSLTSEDSAVYYCA	R	E	G	102
89	J558.5*	61	.....	T.	.....	.....	.....	98
89	45.21.1*	61	.....	T.	.....	G.	.....	98
87	J558.11*	61	.....	T.	.....	H.S.	.....	98
88	AAC35164	61	.....	.....	N.	.....	T	102
86	AAC03071	61	.....	.....	G.	.....	R	102
86	1A6T D	61	.....	.....	G.	.....	R	102
86	1A6T B	61	.....	.....	G.	.....	R	102



83	AAH55910	80	.....	.T.....	.....N.....	.....	YYY---S---S-	124
84	BAC10641	61	.....	.T.....	.....	.....	---R-D---MD-	102
82	CAD32498	80	...E.	.T.....	.....	.....	---G---LH-	121
82	CAD32497	80	...E.	.T.....	.....	.....	---G---LH-	121
83	CAA80023	61	.....	.T.....	.....H.....	.....	---R---TT	103
85	AAA51044	64	.....	.....	.....I.....	.....T	---A-T---FG-	105
84	AAO89516	60	...T.	.....	.....	.....F.....	---RNFA---LD-	103
82	CAB65236	61	.....	.T.....	.....Q.N.....	.....	---D-K---D.Y	103
83	AAB53405	80	.....	.T.....	.....	.....KGLP.	---Y-Y---FD-	125
79	I37267	65	.....	.T.....	.....	.....	---R---LTT	107
87	AAQ74666	53	.....	.....	.....	.....V---	---G---YLGAMD-	98
81	CAB65237	61	.....	.T.....	.....Q.N.....	.....	---D-R---Y.A	103
80	AAB03592	61	.....	.T.....	.....H.....	.....	---G---N.P	103
82	P01757	61	.....	.T.....	.....Q.N.....	.....	---D-R---	101
82	MHMSJ5	61	.....	.T.....	.....Q.N.....	.....	---D-R---	101
82	AAA37775	78	.....	.T.....	.....Q.N.....	.....	---D-S---N.Y	120
81	AAD47037	61	.....	.T.....	.....	.....K	---KVR---Y.A	105
79	CAA80045	61	.....	.T.....	.....L.....Q.N.....	.....	GETTVGK---Y.F	110
81	CAA80085	61	.....	.T.....	.....L.....Q.N.....	.....	---D---Y.G	103
82	AAA38518	61	.....	.T.....	.....H.....	.....YY---	---D---TFD	105
82	AAA37776	78	.....	.T.....	.....Q.N.....	.....	---D-Y---S.V	120
GL ID#								
ND	QUERY	103	-----	W---	WGHGTLTVSS	114		
89	J558.5*		-----					
89	45.21.1*		-----					
87	J558.11*		-----					
88	AAC35164	103	-----	Y----	Q.PV....	114		
86	AAC03071	103	-----	YFDF..	Q.S.....	117		
86	1A6T D	103	-----	YFDF..	Q.S.....	117		
86	1A6T B	103	-----	YFDF..	Q.S.....	117		
83	AAH55910	125	-----	YFDV..	A.V....	140		
84	BAC10641	103	-----	Y----	Q.SV....	114		
82	CAD32498	122	-----	FPY..	Q.LV..A	136		
82	CAD32497	122	-----	FPY..	Q.LV..A	136		

83	CAA80023	104	VFD-----Y-----..Q.....	118
85	AAA51044	106	-----Y-----..Q..LV...A	117
84	AAO89516	104	-----Y-----..Q..V....	115
82	CAB65236	104	FD-----Y-----..Q.....	117
83	AAB53405	126	-----Y-----..Q.....	137
79	I37267	108	VVAKSYFPDY-----..Q.....	128
87	AAQ74666	99	-----Y-----..Q..SV....	110
81	CAB65237	104	MD-----Y-----..Q..SV....	117
80	AAB03592	104	YYYAMD--Y-----..Q..SV....	121
82	P01757	102	-----YFPDV..A..V....	117
82	MHMSJS	102	-----YFPDV..A..V....	117
82	AAA37775	121	FD-----Y-----..Q.....	134
81	AAD47037	106	MD-----Y-----..Q..SV....	119
79	CAA80045	111	D-----Y-----..Q.....	123
81	CAA80085	104	SNFD-----Y-----..Q.....	118
82	AAA38518	106	-----Y-----..Q.....	117
82	AAA37776	121	FD-----Y-----..Q.....	134